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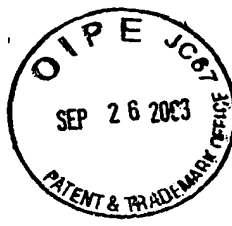
1/15

1 GNTCTAGAANTA GTGGATCCCCC GGGTGCGAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
 CNAGATCTTNAT CACCTAGGGGG CCCGACGTCTT AAGGTGCCGGG GACCTCCCGAG ACCACCCCGACT
 73 GCGCTCTCCGC GGGGCGCGGGG ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGCA TCAGCTACCGGG
 CGCGAGACGGG CCCCCGCGCCG TGTCGTCTTCG TCCAGCGCACC CGCAGACCCCGT AGTCGATGGCCC
 145 GTGTCGGGCT GAAGAGCCAGG AGCCAAGGCAGC CACCCCGGGGG TGGCGACCTTG GGGAGTTGGTG
 CACCAGGCCCGA CTTCTCGTCCG TCGTTCCGTCG GTGGGGCCCCC ACCGCTGAAAC CCCCTCAACCAC
 217 CCCCCCCCCA GGCTTGCGGG GTCATGGGGCCC CCCCATTCTGG CCGGGGGCGGTG CGAGTCGGGGCC
 GGGCGGGGGT CCGGAACCGCCC CAGTACCCCGG GGGGTAAGACCC GGGCCCCCGCAC GCTCAGCCCCCG
 1 MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla
 289 CTGCTGCTGCTG GGGGTTTGGG CTGGTGTCTGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
 GACGACGACGAC CCCCCAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
 16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn
 361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
 TTCTCCAAGGTC CGTCTCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
 40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro
 433 CGGGCCCCGCCT CCTGGCCCTCAC TCCTCTCCIAAT TATGAGTTCTAC AAGCTGTACCCTG GTAGGGGGTGCT
 GCCCGGGCCGGA GGACGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCACGA
 64 ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla
 505 CAGGGCCGGCGC TGTAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
 GTCCCGGCGCGG ACACCTCGTGGG GGACGGGGTTG GAGGAAGAGTGA ACACCTAGCGGGT CTGGACCTAGAG
 88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu
 577 CGCTTACCATC AAGTTCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTCCGCTCG CACCACGATTAC
 GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCGAAGCGGAGC GTGGTGCTAATG
 112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr

FIG. 1A

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169 TACATCATTGCC ACATCGGATGGG ACCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
 136 ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
 TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg
 721 GGCATGAAGGTG CTTCTCCAGTG GGACAAAGTCCC CGAGGAGGGGT GTCCCCCGAAAA CCTGTGTCTGAA
 CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCGA CAGGGGCTTTT GGACACAGACTT
 160 GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu
 793 ATGCCCCATGGAA AGAGACCGAGGG GCAGCCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
 TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTG CGACCTCGGACCC TTCTCTCTGGAC GGTCCACTGGGG
 184 MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro
 865 ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
 TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
 208 ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla
 937 GCAGGGGGGCTG GCGTGTCTTTG CTGGCGGTGGCA GGGGTGGGGT GCCATGTGTTGG CGGAGACGGCGG
 CGTCCCCCGAC CGCGACGAGAAC GACCCGACCGT CCGCGACCCCA CGGTACACAACC GCCTCTGCCGCC
 232 AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg
 1009 GCCAAGCCTTCG GAGATCGCCAC CCTGGTCTTGG TCCTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
 CCGTTCGGAAGC CTCTACGGGTG GGACCGAGCCG AGGAAGCCCTCC CCTCCAGAGAC CCGACCCCCCA
 256 AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly
 1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GCGGGGGCTGCA
 CCTCCACCCCTAC CCGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
 280 GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla
 1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
 CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCTTA
 304 AspProProphe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp
 1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACACA TCGATTTCTGTG TTGGAGTGGCCC ATATTGCATACG
 CCGGGGGGGTC TCGGAGGTTTG TAGATGATGTGT AGCTAAAGACAC AACCTCACCGGG TATAACGTATGC
 328 GlyProProGln SerProProAsn IleTyrTyrThr SerIleSerVal LeuGluTrpPro IleLeuHisThr

FIG. 1B

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1297 ATACAACTGTTT TTCAATCGGATCC AAGTGCTCCCGT GTCACATACATTC TTATTTCCCTGTG CAAGTTATTACG
TATGTTGACAAA AAGTACGCTAGG TTCACGAGGGCA CAGTGATGTAAG AATAAAGGACAC GTTCAATAATGC
352 IleGlnLeuPhe PheMetArgSer LysCysSerArg ValThrThrPhe LeuPheProVal GlnValIleThr
1369 ACATCGACTTGC CGGATGACTTCA TTTAGCTTTACC ACCCTGAACCCA TCCATGCAGGCC TGCAGAGCACAG
TGAGCTGAACG GCCTACTGAAGT AAATCGAAATGG TGGGACTTGGGT AGGTACGTCCGG ACGTCTCGTGTC
376 ThrSerThyCys ArgMetThrSer PheSerPheThr ThrLeuAsnPro SerMetGlnAla CysArgAlaGln
1441 ATGGGGGAATTC CGAATCAGATGG TGTTTCTGGGG GACAGGATCCTG GGTACGGCTCTG TTTGTGCTTGTG
TACCCCTTAAG GCTTAGTCTACC ACAAGACCCCC CTGTCTTAGGAC CCATGCCGAGAC AAACACGAACAC
400 MetGlyGluPhe ArgIleArgTrp CysPheTrpGly AspArgIleLeu GlyThrAlaLeu PheValLeuVal
1513 CTTATTCTTCTT CTGGGAGGCTG AATATGCATCAG ACGACACTGCTC CGGCAACGGGC AGTGTGGAGGCG
GAATAAGAAGAA GAACCTCCGAC TTATACGTAGTC TGCTGTGACGAG GCCGTTGCCCGG TCACACCTCCGC
424 LeuIleLeuLeu LeuGlyArgLeu AsnMetHisGln ThrThrLeuLeu ArgGlnArgAla SerValGluAla
1585 GAAGCCGGCCAG CATGTCCTCCCTG TGATAGGATTGA AAGAGCTACTGA GAATAGGGGGCT TCTCAATGAGAG
448 CTTGGCCCGGTC GTACCAGGGGAC ACTATCCTAACT TTCTCGATGACT CTTATCCCCCGA AGAGTTACTCTC
GluAlaGlyGln HisGlyProLeu (SEQ ID NO: 2)
1657 AGCGGAGGCTGC TGTTATCATGGG AACCAGGCAGAT CAATCATCCCTG GCAGGTCAGGCA GGAAGTTACTTA
TCGCCTCCGACG ACAATAGTACCC TTGGTCCGTCTA GTTAGTAGGGAC CGTCCAGTCCGT CCTTCAATGAAT
1729 GCTTCTCCTTCA CCTTCTTCCCAC AGAATTATTAT AGGCTTGTTCCA AGTTGTAGTGTG TGATCAGATTCTG
CGAAGAGGAAGT GGAAGAAGGGTG TCTTAAATAATA TCCGAACAAGGT TCAACATCACAC ACTAGTCTAAGC
1801 TGCTGCCTGTCA GCTCTGTGCTAC CTGGCAGTTCCC CTCATGGAATTC GATATCAAGCTT ATCGATACCGTC
ACGACGGACAGT CGAGACACGATG GACCGTCAAGGG GAGTACCTTAAG CTATAGTTGAA TAGCTATGGCAG
1873 GACCT (SEQ ID NO: 1)
CTGGA

FIG. 1C

FIG. 1A

FIG. 1B

FIG. 1C

FIG. 1

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1 GNTCTAGAANTA GTGGATCCCCC GGGCTGCAGGAA TTCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
CNAGATCTTNAT CACCTAGGGGG CCGACGTCCTT AAGGCTGCCGG GACCTTCCCGAG ACCACCCCGACT

73 GCGCTCTGCCG GGGGGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGCA TCAGCTACCGGG
CGCGAGACGGC CCCCCGCGCCG TGTCGTCCTCG TCCAGGCGCACC CCGACCCCGCGT AGTCGATGGCCC

145 GTGGTCCGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGG TGGCGCACTTG GGGGAGTTGGTG
CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTG GTGGGGCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCCGCCCCCA GGCCTTGGCGG GTCATGGGCC CCCCATTTCTGG CCGGGGGCGGTG CGAGTCGGGGCC
GGGGGGGGGT CCGGAACCGCCC CAGTACCCCGG GGGTAAGACCC GGGCCCCCGCAC GCTCAGCCCCGG
1 MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGTTTTGGGG CTGGTGTCTGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA

16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
TTCTCCAAGGTC CGTCTCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG

40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CCGGCCCCGCCT CTTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA

64 ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTAGGCACCC CTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCC GACCTGGATCTC
GTCCCGGGCCGG CACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA AACTAGCGGGT CTGGACCTAGAG

88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTTCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTCCGCTCG CACCACGATTAC
GCGAAGTGCTAG TTCAAGGTCTC ATATCGGGATTA GAGACCCCGGTG CTCAGGCGGAGC GTGGTGCTAATG

112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr

FIG. 2A

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649 TACATCATTTGCC ACATCGGATGGG ACCCGGGAGGGG CTGGAGAGCCTG CAGGAGGGTGTG TGCCTAACACAGA
 ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
 136 TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg
 721 GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
 CCGTACTTCCAC GAAGAGGCTCAC CTTGTTTCAGGG GCTCCTCCCCGA CAGGGGCTTTT GGACACAGACTT
 160 GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu
 793 ATGCCCCATGGAA AGAGACCGAGGG GCAGCCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
 TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTG GACCTCGGACCC TTCCTCTTGGAC GTCCACTGGGG
 184 MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro
 865 ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCCTGCA GTGGCTGGGGCA
 TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCCGT
 208 ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla
 937 GCAGGGGGGCTG GCGCTGCTCTTG CTGGCGTGGCA GGGGCTGGGGT GCCATGTGTTGG CGGAGACGGCGG
 CGTCCCCCGAC CGCGACGAGAAC GACCGCACCCGT CCGGACCCCCA CCGTACACAACC GCCTCTGCCGCC
 232 AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg
 1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCITGG TCCTTCGGGAGG GGAGGGTCTCTG GGCTGGGGGGT
 CGGTTCCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
 256 AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly
 1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGT GGCGGGGCTGCA
 CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
 280 GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla
 1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
 CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCCTA
 304 AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp
 1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACAAG GTATGAGGGCTC TTGAGTGGCCC ATATTGCATACG
 CCGGGGGGGTTC TCGGGAGGTTTG TAGATGATGTTT CATACTCCCGAG AACCTCACCGGG TATAACGTATGC
 328 GlyProProGln SerProProAsn IleTyrTyrLys ValOP* (SEQ ID NO: 4)

FIG. 2B

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1297 AGCCCTTCTTGG GGTGCTCCTCCA GTTTAATTCCTG GTTTGAGGGACA CCTCTAACATCT CGGCCCCCTGTG
 TCGGAAGAACC CCACGAGAGGT CAAATTAAGGAC CAACTCCCTGT GGAGATTGTAGA GCCGGGGGACAC

 1369 CCCCCCAGCCC CTTCACTCCTCC CGGCTGCTGTCC TCGTCTCCACTT TTAGGATTCTT AGGATTCCCACT
 GGGGGGTCTGG GAAGTGAGGAG GCCGACGACAGG AGCAGAGGTGAA AATCCTAAGGAA TCCTAAGGGTGA

 1441 GCCCCACTTCCT GCCCTCCCGTT GGCCATGGGTGC CCCCCTCTGTCT CAGTGTCCCTGG ATCCTTTTCTCT
 CGGGTGAAGGA CGGGAGGGCAAA CCGGTACCCACG GGGGAGACAGA GTCACAGGGACC TAGGAAAAAGGA

 1513 TGGGAGGGGCA CAGGCTCAGCCT CCTCTCTGACCA TGACCCAGGCAT CCTTGTCCCTCT CACCCACCCAGA
 ACCCTCCCCGT GTCCGAGTCGGA GGAGAGACTGGT ACTGGGTCCGTA GGAACAGGGGGA GTGGGTGGGTCT

 1585 GCTAGGGGCGGG AACAGCCACCT TTTGGTTGGCAC CGCCTTCTTTCT GCCTCTCACTGG TTTTCTCTTCTC
 CGATCCCCGCC TTGTGGGTGGA AAACCAACCGTG GCGGAAGAAAGA CCGAGAGTGACC AAAGAGAAGAG

 1657 TATCTCTTATTC TTTCCCTCTCTT CCGTCTCTAGGT CTGTTCTTCTTC CCTAGCATCCTC CTCCCCACATCT
 ATAGAGAATAAG AAAGGGAGAGAA GGCAGAGATCCA GACAAGAAGAAG GGATCGTAGGAG GAGGGTGTAGA

 1729 CCTTACCCCTC TTGGCTTCTTAT CCTGTCCCTCTC CCATCTCCTGGG TGGGGGCATCAA AGCATTTCTCCC
 GGAAAGTGGAG AACCGAAGAATA GGACACGGAGAG GGTAGAGGACCC ACCCCCGTAGTT TCGTAAAGAGGG

 1801 CTTAGCTTTCAG CCCCCCTTCTGA CCTCTCATACCA ACCACTCCCCCTC AGTCTGCCAAAA ATGGGGCCCTTA
 GAATCGAAAGTC GGGGGGAAGACT GGAGAGTATGGT TGGTGAGGGGAG TCAGACGGTTTT TACCCCGGGAAT

 1873 TGGGGAAGGCTC TGACACTCCACC CCAGCTCAGGCC ATGGGCACCAGG GCTCCATTCTCT GGCCTGGCCCCAG
 ACCCTTCCGAG ACTGTGAGGTGG GGTGAGTCCGG TACCCGTCGTCC CGAGGTAAGAGA CCGGACCGGGTC

 1945 GCCTCTACATAC TTACTCCAGCCA TTTGGGTGGTT GGGTCATGACAG CTACCATGAGAA GAAGTGTCCCGT
 CGGAGATGTATG AATGAGTCTGGT AAACCCCAACCA CCCAGTACTGTC GATGGTACTCTT CTTACAGGGCA

 2017 TTTGTCCSGTGG CCAATAGCAAGA TATGAACCGGTC GGGACATGTATG GACTTGGTCTGA TGCTGAATGGGC
 AACAGGTCACC GGTATCGTTCT ATACTTGGCCAG CCCTGTACATAC CTGAACAGACT ACGACTTACCCG

FIG. 2C

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2089 CACTTGGACCG GAAGTGACTTGC TCCAGACAAGAG GTGACCAGGCCG GGACAGAAATGG CCTGGGAAGTAG
GTGAACCCCTGGC CTTCACTGAACG AGGTCTGTTCTC CACTGGTCCGGG CCTGTCTTTACC GGACCCCTTCATC
2161 CAGAAGCAGTGC AGCAGGAACTGG AAGTGCCCTTCAT CCAGGACAGGAA GTAGCACTTCTG AAACAGGGAAGTG
GTCTTCGTCACG TCGTCCCTTGACC TTCACGGAAGTA GGTCCTGTCTT CATCGTGAAGAC TTTGTCTCTTAC
2233 GTCTGGCTGGAA CTCCAAGTGGCT TAGTCTGGGGGA TCAGGAGGTGGG AGGTGGATGGT CTTATTCTGTGG
CAGACCGACCTT GAGGTTACCGA ATCAGACCCCTT AGTCTCCACCC TCCACCTACCAA GAATAAGACACC
2305 AGAAGAAGGGCG GGAAGAAGTCTTCC TTTCAGGAGGAA GCTGGAACCTTAC TGACTGTAAGAG GTTAGAGGTGGA
TCTTCTTCCCGC CCTTCTTGAAGG AAAGTCCCTCCTT CGACCTTGAATG ACTGACATTCTC CAATCTCCACCT
2377 CCGA (SEQ ID NO: 3)
GGCT

FIG. 2D

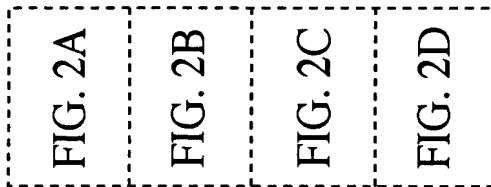


FIG. 2

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AL-2b.L	1	GNTCTAGAA	NTAGTGGAT	CCCCCGGGCT	GCAAGGA	ATTCGGA	CGGCCCT
AL-2b.L	51	GGAAGGGCT	CTGGTGGGGCT	GAGCGCT	CTGCCGCGGGG	CGCGGCA	CAG
AL-2b.L	101	CAGGAAGCA	AGGTCCGCGT	GGGCGCT	GAGGCA	TACGCT	ACCGGGTGGTC
AL-2b.L	151	CGGGCTGA	AGAGCCAGGCA	AGCCAGGCA	AGCCAGGCGG	GTGGCGAC	
AL-2b.L	201	TTTGGGGAG	TTGGTGCC	CCCGCCAGG	CCCTTGGC	GGGTCA	TGGGGC
AL-2b.L	251	CCCCCAT	TCTGGCCGGG	CGGTGCGAG	TGCGGCCCT	GTGCTGCTG	
AL-2b.L	301	GGGGTTT	TGGGCTGGT	GCTGCGCT	GAGCCTG	TCTACTGGA	
AL-2b.L	351	CTCGGCGA	ATAAGAGG	TCCAGGCA	AGGGTGGT	TATGTGCT	TACCTC
AL-2b.L	401	AGATCGGG	AGCCGGCT	AGACCTG	CTCGCCCGG	CCCGGCT	TCCTGGC
AL-2b.L	451	CCTCACT	CCTCCTA	ATTATGAG	TTCTACA	AGCTGTAC	CTGGTAGGGG
AL-2b.L	501	TGCTCAGG	GCCGG	CGCTGTGAG	GCACCCCT	TGCCCCAA	ACCTTCTCA
HI0006	1	- - - - -	GCCG	ACGCTGTGAG	GCACCCCT	TGCCCCAA	ACCTTCTCA
AL-2b.L	551	CTTGTGAT	CGCCCA	GACCTGGAT	CTCCGCT	TCACCA	TCAAGTCCAGGAG
HI0006	43	CTTGTGAT	CGCCCA	GACCTGGAT	CTCCGCT	TCACCA	TCAAGTCCAGGAG
AL-2b.L	601	TATAGCCC	TAACTCT	CTGGGCC	ACGAGT	TCGCTCGC	ACCACTTACTA
HI0006	93	TATAGCCC	TAACTCT	CTGGGCC	ACGAGT	TCGCTCGC	ACCACTTACTA
AL-2b.L	651	CATCAT	TGCCACAT	CGGATGGG	ACCCGGGAGG	CTGGAGAG	CCCTGCAGG
HI0006	143	CATCAT	TGCCACAT	CGGATGGG	ACCCGGGAGG	CTGGAGAG	CCCTGCAGG
AL-2b.L	701	GAGGTGT	GTGCTTAA	CCAGAGG	CAATGAAGG	TGCTTCT	CCGAGTGGGACAA
HI0006	193	GAGGTGT	GTGCTTAA	CCAGAGG	CAATGAAGG	TGCTTCT	CCGAGTGGGACAA

FIG. 3A

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AL-2b.L 751 AGT C C C C G A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C C C A T
H10006 243 AGT - C C C G A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C C C A T

AL-2b.L 801 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T - G G A G C C T - G G G A A G G A G A A
H10006 292 G G A A A G A G A C C G A G G G G C A G C C C A C A G C C T G G G A G C C T G G G G A A G G A G A A

AL-2b.L 849 C C T G C C A G G T G A C C C C A C C A G C A A T G C A A C C T C C C G G G T - - G C T G A A G G
H10006 342 C C T G C C A G G T G A C C C C A C C A G C A A T N C A A C C T T C C G G G G T T G C T T G A A G G

AL-2b.L 897 C C C C C T - - G C C C C C C T C C C C A G C A - T G C C C T G C A G T - - G G C T G G G G C A G C A G G
H10006 392 G C C C C T T G A C C C T T T C C C A G C A T T G C N T G C A N T T G G T T N G G G G C A G C A N G

AL-2b.L 942 G G G G C - - - T G G C G C T G C T C T T G C T G G G C G T G G C A G G G G C T G G G G G T G C C
H10006 442 G G G G N G T T T T G G C (SEQ ID NO: 5)

AL-2b.L 988 A T G T G T T G C G G A G A C G G C G G G C C A A G C C T T C G G A G A G T C G C C A C C C T G G

AL-2b.L 1038 T C C T G G C T C C T T C G G G A G G G A G G T C T C T G G C C T G G G G G T G G A G G T G

AL-2b.L 1088 G G A T G G G A C C T C G G G A G G C T G A G C C T G G G G A G C T A G G G A T A G C T C T G C G G

AL-2b.L 1138 G G T G G C G G G C T G C A G A T C C C C C C T T C T G C C C C A C T A T G A G A A G G T G A G

AL-2b.L 1188 T G G T G A C T A T G G G C A T C C T G T G T A T A T C G T G C A G G A T G G G C C C C C C A G A

AL-2b.L 1238 G C C C T C C A A C A T C T A C A C A T C G A T T T C T G T G T T G G A G T G G C C C A T A

AL-2b.L 1288 T T G C A T A C G A T A C A A C T G T T T T T C A T G C G A T C C A A G T G C T C C C G T G T C A C

FIG. 3B



AL-2b.L1338 T A C A T T C T T A T T T C C T G T G C A A G T T A T T A C G A C A T C G A C T T G C C G G A T G A
AL-2b.L1388 C T T C A T T T A G C T T T A C G A C C C T G A A C C C A T C C A T G C A G G C C T G C A G A G C A
AL-2b.L1438 C A G A T G G G G A A T T C C G A A T C A G A T G G T G T T T C T G G G G G A C A G G A T C C T
AL-2b.L1488 G G G T A C G G C T C T G T T T G T G C T T G T G C T T A T T C T T C T T G G G A G G C T G A
AL-2b.L1538 A T A T G C A T C A G A C G A C A G T G C T C C G G C A A C G G G C C A G T G T G G A G G C G G A A
AL-2b.L1588 G C C G G C C A G C A T G G T C C G C T G T G A T A G G A T T G A A A G A G C T A C T G A G A A T A
AL-2b.L1638 G G G G G C T T C T C A A T G A G A G A G C G G A G G C T G C T G T T A T C A T G G G A A C C A G G
AL-2b.L1688 C A G A T C A A T C A T C C C T G G C A G Q T C A G G C A G G A A G T T A C T T A G C T T C T C C T
AL-2b.L1738 T C A C C T T C T T C C C A C A G A A T T A T T A T A G G C T T G T T C C A A G T T G T A G T G T
AL-2b.L1788 G T G A T C A G A T T C G T G C T G C C T G T C A G C T C T G T G C T A C C T G G C A G T T C C C C
AL-2b.L1838 T C A T G G A A T T C G A T A T C A A G C T T A T C G A T A C C G T C G A C C T (SEQ ID NO: 1)

FIG. 3C

FIG. 3A
FIG. 3B
FIG. 3C

FIG. 3

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lerk2 1 MA - RP GQR WL G KW L VAMV VWA L CRL A T P L A K N L E P V S W S L N P K F L S G K G
 huHTKL 1 MAV R R D S V W K Y C W G V L M V - - - L C R T A I S K S I V L E P I I Y W N S S N S K F L P G Q G
 AL2.sht 1 MG - P P H S G P G G V R V G A L L L G V L G L V S G L - - - S L E P V Y W N S A N K R F Q A E G G
 AL2.long 1 MG - P P H S G P G G V R V G A L L L G V L G L V S G L - - - S L E P V Y W N S A N K R F Q A E G G

lerk2 50 LV I I Y P K I G D K L D I I C P R A - - - E A G R - - - P Y E Y Y K L Y L V R P E Q A A C S T V L D
 huHTKL 48 LV L Y P Q I G D K L D I I C P K V - - - D S K T V G Q Y E Y Y K V Y M V D K D Q A D R C T I K K E
 AL2.sht 48 Y V L Y P Q I G D R L D L L C P R A R P P G P H S S P N Y E F Y K L Y L V G G A Q G R R C E A P P A
 AL2.long 48 Y V L Y P Q I G D R L D L L C P R A R P P G P H S S P N Y E F Y K L Y L V G G A Q G R R C E A P P A

lerk2 95 P N V L V T C N R P E Q E I R F T I K F Q E F S P N Y M G L E F K K H H D Y Y I T S T S N G S L E G
 huHTKL 95 N T P L L N C A K P D Q D I K F T I K F Q E F S P N L W G L E F Q K N K D Y Y I I S T S N G S L E G
 AL2.sht 98 P N L L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H D Y Y I I A T S D G T R E G
 AL2.long 98 P N L L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H D Y Y I I A T S D G T R E G

lerk2 145 L E N R E G G V C R T R T M K I I M K V G Q D P N A V T P E Q L T T S R P S K E A D N T V K M A T Q
 huHTKL 145 L D N Q E G G V C Q T R A M K I L M K V G Q D A S S - - - - - A G S T R N K D P T R R P E L E A G
 AL2.sht 148 L E S L Q G G V C L T R G M K V L L R V G Q S P R G G A V P R K P V S E M P M E R D R G A A H S L E
 AL2.long 148 L E S L Q G G V C L T R G M K V L L R V G Q S P R G G A V P R K P V S E M P M E R D R G A A H S L E

FIG. 4A

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lerk2 195 A P G S R G S L G D S D G K H E T V N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A A V
huHTKL 189 T N G - R S S T T S P F V K P N P G S S T D G N S A G H S G - - - - - N N I L G S E V A L F A G I
AL2.sht 198 - P G K E N L P G D P T S N A T S R G A E G P L P P S M P A V A G A A G G L - - - A L L L L G V A
AL2.long 198 - P G K E N L P G D P T S N A T S R G A E G P L P P S M P A V A G A A G G L - - - A L L L L G V A

lerk2 245 G A G C V I F L L I I I F L T V L L L K L R K R H R K H T Q - Q R A A A L S L S T L A S P K G G S G
huHTKL 232 A S G C I I F I V I I I T L V V L L L K Y R R R H R K H S P - Q H T T T L S L S T L A T P K R S G N
AL2.sht 244 G A G G A - - - - - M C W R R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - G G G M G
AL2.long 244 G A G G A - - - - - M C W R R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - - G G G M G

lerk2 294 T A G T E P S D I I I P L R - - - T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
huHTKL 261 N N G S E P S D I I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S P A
AL2.sht 265 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P
AL2.long 295 P R E A E P G E L G I A L R G G G A A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S P P

lerk2 341 N I Y Y - - - - -
huHTKL 328 N I Y Y - - - - -
AL2.sht 335 N I Y Y - - - - -
AL2.long 335 N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M T S F

FIG. 4B

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lerk2	345	- - - - -	- - - - -	KV	(SEQ ID NO: 9)
huHTKL	332	- - - - -	- - - - -	KV	(SEQ ID NO: 10)
AL2.sht	339	- - - - -	- - - - -	KV	(SEQ ID NO: 4)
AL2.long	385	S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N M H			

AL2.long 435 Q T T L L R Q R A S V E A E A G Q H G P L (SEQ ID NO: 2)

FIG. 4C

FIG. 4A

FIG. 4B

FIG. 4C

FIG. 4



LERK2	1	MA	-	RP	QR	WL	SK	WL	VAM	V	LT	LC	RL	AT	PL	AK	NL	EP	VS	WS	SL	NP	K	FL	SG	KG																			
huHTKL	1	MA	V	R	RD	SV	WK	Y	CM	GV	LM	V	LC	RT	AI	SK	SI	VL	EP	I	YW	NS	SK	FL	PG	QG																			
AL2.long	1	MG	PP	HS	GP	-	GG	VR	GA	LL	L	-	LG	VL	GL	VS	GL	SL	EP	VY	WNS	AN	KR	FF	QA	EG																			
LERK2	50	LV	I	YP	KI	GD	K	L	D	I	CP	RA	-	-	-	E	AG	R	-	-	PY	EY	YK	LY	VR	PE	QA	AA	CS	TV	LD														
huHTKL	48	LV	Y	P	Q	I	GD	K	L	D	I	CP	KV	-	-	-	DS	KT	VG	QY	EY	YK	VY	VM	V	DK	QAD	RC	T	I	KK														
AL2.long	48	YV	LY	P	Q	I	GD	R	LD	LL	CP	RA	RP	PG	PH	SS	PN	YE	FY	K	LY	LV	GG	QA	QGR	RC	EA	PP	A																
LERK2	95	PN	V	LV	TC	N	K	P	H	QE	I	R	FT	I	K	F	Q	E	F	SP	NY	M	G	L	E	FK	YH	D	Y	Y	I	TS	NS	GS	LE	G									
huHTKL	95	NT	PL	LL	NC	A	K	P	D	Q	D	I	K	FT	I	K	F	Q	E	F	SP	N	L	W	G	L	E	FQ	KN	K	D	Y	I	IS	TS	NS	GS	LE	G						
AL2.long	98	PN	LL	TC	D	R	P	D	L	DL	R	FT	I	K	F	Q	EY	SP	N	L	W	GH	E	FR	SH	H	D	Y	I	IA	TS	D	G	T	RE	G									
LERK2	145	LE	N	REG	GV	C	R	TR	TM	KI	V	M	K	V	G	Q	DP	NA	VT	PE	Q	LT	TS	RP	SK	ES	DN	TV	K	T	A	T	Q												
huHTKL	145	LD	N	Q	EG	V	C	Q	TR	AM	KI	L	M	K	V	G	Q	DA	SS	-	-	-	-	AG	ST	R	N	K	D	P	T	RR	P	E	LE	AG									
AL2.long	148	LE	S	L	Q	GG	V	C	L	TR	GM	K	V	L	R	V	G	Q	SP	R	G	-	-	-	-	GA	V	P	R	K	P	V	S	EM	P	ME	R	DR	G						
huHTKL	195	A	P	G	R	G	S	Q	G	D	S	D	G	K	H	E	T	V	N	Q	E	E	K	S	GP	GA	GG	S	G	D	S	D	S	F	F	N	S	K	V	A	L	F	A	V	G
AL2.sht	189	T	N	G	R	S	S	T	T	S	P	F	V	K	P	N	P	GS	S	T	D	G	N	S	A	GH	SG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AL2.long	192	A	A	H	S	L	E	P	G	K	E	N	L	P	G	D	P	TS	N	A	T	S	R	GA	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

FIG. 5A

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LERK2 245 AGCVIFLLIIIFLTVLLKLRKRHRKHTQQRAAALSLSSTLASPKGGS
huHTKL 233 SGCIIIFIVIIITLVVLLKYRRRRHRKHSPQHITTTLSLSTLATPKRSG
AL2.long233 GGLALLLGVAGAGAMCWRRRRAKPSERHPPGSGFGRGGSLLGLGGGG

LERK2 292 -GTAGTEPSDIIIPLR--TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS
huHTKL 280 -NNNGSEPSDIIIPLR--TADSVFCPHYEKVSGDYGHPVYIVQEMPPQS
AL2.long283 MGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGP

LERK2 338 PANIYY-----
huHTKL 326 PANIYY-----
AL2.long333 PPNIYYTSISVLEWPI LHTIQ LFFMRSKCSRVT TFLFPVQVIT TSTCRMT

LERK2 344 -----KV----- (SEQ ID NO: 9)
huHTKL 332 -----KV----- (SEQ ID NO: 10)
AL2.long383 SFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALFVLVLI LLLGR LN

AL2.long433 MHQTTLLRQRASVEAEAGQHGPL (SEQ ID NO: 2)

FIG. 5B

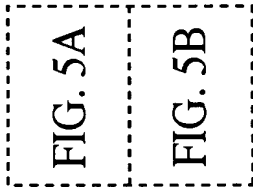


FIG. 5

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